

SEQUENCE LISTING

<110> Viaxxel Biotech GmbH

<120> Compounds that affect CD83 expression, pharmaceutical compositions comprising said compounds and methods for identifying said compounds

<130> 84201

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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25

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ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc 144

Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser

45

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Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
85 90 95

Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
115 120 125

Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu

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130              135              140

Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
145              150              155              160

Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
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Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
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tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag      145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
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Thr Leu Pro Lys Thr Glu Thr Val

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35 40 45

Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu

50 55 60

Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala

65 70 75 80

Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
 85 90 95

Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
 100 105 110

Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
 115 120 125

Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
 130 135 140

Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
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Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
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Thr Glu Thr Val
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<222> (1)..(978)

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 165 170 175

gag ccc atc gca gtg aag ttt gca gcc aac ccc aac cag aac aaa aac 576
 Glu Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln Asn Lys Asn
 180 185 190

gtg gca ctc ctc tcg cag ctg tac cac tcg cca gcg cga cgg ttc gga 624
 Val Ala Leu Leu Ser Gln Leu Tyr His Ser Pro Ala Arg Arg Phe Gly
 195 200 205

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 Gly Pro Val His His Gln Ala Gln Arg Phe Arg Phe Ser Pro Met Gly
 210 215 220

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 225 230 235 240

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 260 265 270

gtg aaa gtg atc cgc gac ttc aac acc aac aag tgc aaa ggg ttt ggc 864
 Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly
 275 280 285

ttt gtg acc atg aca aac tat gaa gaa gcc gcg atg gcc ata gcc agc 912
 Phe Val Thr Met Thr Asn Tyr Glu Glu Ala Ala Met Ala Ile Ala Ser

1003367-41901
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 35 40 45

Ala Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly
 50 55 60

Phe Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr
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Leu Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala
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Arg Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly
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Gly Pro Thr Thr Ile Asn Asn Asn Cys Ser Ser Pro Val Asp Ser Gly

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aac aca gaa qac aqc aaq acc aac tta ata qtc aac tac ctt cct caq 144

Asn Thr Glu Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln

35 40 45

aac atg aca cag gag gaa cta aag agt ctc ttt ggg agc att ggt gaa 192

Asn Met Thr Gln Glu Glu Leu Lys Ser Leu Phe Gly Ser Ile Gly Glu

50 55 60

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65 70 75 80

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Gly Tyr Gly Phe Val Asn Tyr Ile Asp Pro Lys Asp Ala Glu Lys Ala

85 90 95

atc aac acc ctg aat gga ttg aga ctt caa acc aaa aca ata aaa gtt 336

Ile Asn Thr Leu Asn Gly Leu Arg Leu Gln Thr Lys Thr Ile Lys Val

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Phe Ser Gln Tyr Gly Arg Ile Ile Thr Ser Arg Ile Leu Val Asp Gln

145 150 155 160

gtc act ggc ata tca agg ggt gta ggg ttt att cga ttt gac aag cga 528
Val Thr Gly Ile Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg

165 170 175

att gag gca gaa gaa gct atc aaa ggc cta aat ggc cag aaa cct ccc 576
Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Pro

180 185 190

ggc gcc acg gag cca atc act gta aag ttt gct aat aac cca agc caa 624
Gly Ala Thr Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln

195 200 205

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210 215 220

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Arg Tyr Pro Gly Pro Leu Ala Gln Gln Ala Gln Arg Phe Arg Leu Asp

225 230 235 240

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245 250 255

att gac gga atg acc agt ttg gct gga att aat atc cct ggg cac cct 816
Ile Asp Gly Met Thr Ser Leu Ala Gly Ile Asn Ile Pro Gly His Pro

260 265 270

Gly Pro Thr Thr Ile Asn Asn Asn Cys Ser Ser Pro Val Asp Ser Gly

20 25 30

Asn Thr Glu Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln
 35 40 45

Asn Met Thr Gln Glu Glu Leu Lys Ser Leu Phe Gly Ser Ile Gly Glu
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Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Gln Ser Leu
 65 70 75 80

Gly Tyr Gly Phe Val Asn Tyr Ile Asp Pro Lys Asp Ala Glu Lys Ala
 85 90 95

Ile Asn Thr Leu Asn Gly Leu Arg Leu Gln Thr Lys Thr Ile Lys Val
 100 105 110

Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr
 115 120 125

Val Ser Gly Leu Pro Lys Thr Met Thr Gln Lys Glu Leu Glu Gln Leu
 130 135 140

Phe Ser Gln Tyr Gly Arg Ile Ile Thr Ser Arg Ile Leu Val Asp Gln
 145 150 155 160

Val Thr Gly Ile Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg
 165 170 175

Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Pro
 180 185 190

Gly Ala Thr Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln
 195 200 205

Lys Thr Asn Gln Ala Ile Leu Ser Gln Leu Tyr Gln Ser Pro Asn Arg
 210 215 220

Arg Tyr Pro Gly Pro Leu Ala Gln Gln Ala Gln Arg Phe Arg Leu Asp

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Pro Ala Gly Pro Ala Leu Pro Asn Gly Pro Leu Leu Gly Thr Asn Gly

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Ala Thr Asp Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln

35 40 45

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Asn Met Thr Gln Asp Glu Phe Lys Ser Leu Phe Gly Ser Ile Gly Asp

50 55 60

atc gag tcc tgc aag ttg gtt cgg gac aag atc aca ggc aga gac ctt 240

Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Arg Asp Leu

65 70 75 80

ggc tac ggg ttt gtg aac tat cct gac ccc aat gat gca gac aaa gcc 288

Gly Tyr Gly Phe Val Asn Tyr Pro Asp Pro Asn Asp Ala Asp Lys Ala

85 90 95

atc aac acc ctc aac ggc ctc aaa tta cag acg aag acc atc aag gtg 336

Ile Asn Thr Leu Asn Gly Leu Lys Leu Gln Thr Lys Thr Ile Lys Val

100 105 110

tcc tat gcc aga ccc agt tca gca tcc atc cgg gat gct aac ctg tac 384

Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr

115 120 125

gtc agc ggg ctc ccc aag acc atg agc cag aaa gag atg gag cag ctc 432

Val Ser Gly Leu Pro Lys Thr Met Ser Gln Lys Glu Met Glu Gln Leu

130 135 140

T06T22 " 134901

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 290 295 300

gtc aag gtc atc cgt gat ttc acc acc aac aag tgc aag ggt ttc ggc 960
 Val Lys Val Ile Arg Asp Phe Thr Thr Asn Lys Cys Lys Gly Phe Gly
 305 310 315 320

ttc gtg acc atg acc aac tat gac gag gcg gcc atg gcc atc gcc agc 1008
 Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Ala Ser
 325 330 335

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 35 40 45

Asn Met Thr Gln Asp Glu Phe Lys Ser Leu Phe Gly Ser Ile Gly Asp
 50 55 60

1003674400

Asn Leu Leu Asn Met Ala Tyr Gly Val Lys Arg Phe Ser Pro Ile Ala
245 250 255

Ile Asp Gly Met Ser Gly Leu Ala Gly Val Gly Leu Ser Gly Gly Ala
 260 265 270

Ala Gly Gly Trp Cys Ile Phe Val Tyr Asn Leu Ser Pro Glu Ala Asp
 275 280 285

Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe Gly Ala Val Thr Asn
 290 295 300

Val Lys Val Ile Arg Asp Phe Thr Thr Asn Lys Cys Lys Gly Phe Gly
 305 310 315 320

Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Ala Ser
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Met Val Met Ile Ile Ser Thr Met Glu Pro Gln Val Ser Asn Gly Pro

1

5

10

15

aca tcc aat aca agc aat gga ccc tcc agc aac aac aga aac tgt cct	96
Thr Ser Asn Thr Ser Asn Gly Pro Ser Ser Asn Asn Arg Asn Cys Pro	
20 25 30	
tct ccc atg caa aca ggg gca acc aca gat gac agc aaa acc aac ctc	144
Ser Pro Met Gln Thr Gly Ala Thr Thr Asp Asp Ser Lys Thr Asn Leu	
35 40 45	
atc gtc aac tat tta ccc cag aat atg acc caa gaa gaa ttc agg agt	192
Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln Glu Glu Phe Arg Ser	
50 55 60	
ctc ttc ggg agc att ggt gaa ata gaa tcc tgc aaa ctt gtg aga gac	240
Leu Phe Gly Ser Ile Gly Glu Ile Glu Ser Cys Lys Leu Val Arg Asp	
65 70 75 80	
aaa att aca gga cag agt tta ggg tat gga ttt gtt aac tat att gat	288
Lys Ile Thr Gly Gln Ser Leu Gly Tyr Gly Phe Val Asn Tyr Ile Asp	
85 90 95	
cca aag gat gca gag aaa gcc atc aac act tta aat gga ctc aga ctc	336
Pro Lys Asp Ala Glu Lys Ala Ile Asn Thr Leu Asn Gly Leu Arg Leu	
100 105 110	
cag acc aaa acc ata aag gtc tca tat gcc cgt ccg agc tct gcc tca	384
Gln Thr Lys Thr Ile Lys Val Ser Tyr Ala Arg Pro Ser Ser Ala Ser	
115 120 125	
atc agg gat gct aac ctc tat gtt agc ggc ctt ccc aaa acc atg acc	432
Ile Arg Asp Ala Asn Leu Tyr Val Ser Gly Leu Pro Lys Thr Met Thr	
130 135 140	
cag aag gaa ctg gag caa ctt ttc tcg caa tac ggc cgt atc atc acc	480
Gln Lys Glu Leu Glu Gln Leu Phe Ser Gln Tyr Gly Arg Ile Ile Thr	
145 150 155 160	
tca cga atc ctg gtt gat caa gtc aca gga gtg tcc aga ggg gtg gga	528

165 170 175

Phe Ile Arg Phe Asp Lys Arg Ile Glu Ala Glu Glu Ala Ile Lys Gly

180 185 190

Leu Asn Gly Gln Lys Pro Ser Gly Ala Thr Glu Pro Ile Thr Val Lys

195 200 205

Phe Ala Asn Asn Pro Ser Gln Lys Ser Ser Gln Ala Leu Leu Ser Gln

210 215 220

Leu Tyr Gln Ser Pro Asn Arg Arg Tyr Pro Gly Pro Leu His His Gln

225 230 235 240

Ala Gln Arg Phe Arg Leu Asp Asn Leu Leu Asn Met Ala Tyr Gly Val

245 250 255

Lys Arg Leu Met Ser Gly Pro Val Pro Pro Ser Ala Cys Ser Pro Arg

260 265 270

Phe Ser Pro Ile Thr Ile Asp Gly Met Thr Ser Leu Val Gly Met Asn

275 280 285

Ile Pro Gly His Thr Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu

290 295 300

Ser Pro Asp Ser Asp Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe

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<211> 380
<212> PRT
<213> Homo sapiens

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Thr Ser Asn Thr Ser Asn Gly Pro Ser Ser Asn Asn Arg Asn Cys Pro
      20                      25                      30
Ser Pro Met Gln Thr Gly Ala Thr Thr Asp Asp Ser Lys Thr Asn Leu
      35                      40                      45
Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln Glu Glu Phe Arg Ser
      50                      55                      60

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Leu Phe Gly Ser Ile Gly Glu Ile Glu Ser Cys Lys Leu Val Arg Asp
65 70 75 80

Lys Ile Thr Gly Gln Ser Leu Gly Tyr Gly Phe Val Asn Tyr Ile Asp
85 90 95

Pro Lys Asp Ala Glu Lys Ala Ile Asn Thr Leu Asn Gly Leu Arg Leu
100 105 110

Gln Thr Lys Thr Ile Lys Val Ser Tyr Ala Arg Pro Ser Ser Ala Ser
115 120 125

Ile Arg Asp Ala Asn Leu Tyr Val Ser Gly Leu Pro Lys Thr Met Thr
130 135 140

Gln Lys Glu Leu Glu Gln Leu Phe Ser Gln Tyr Gly Arg Ile Ile Thr
145 150 155 160

Ser Arg Ile Leu Val Asp Gln Val Thr Gly Val Ser Arg Gly Val Gly
165 170 175

Phe Ile Arg Phe Asp Lys Arg Ile Glu Ala Glu Glu Ala Ile Lys Gly
180 185 190

Leu Asn Gly Gln Lys Pro Ser Gly Ala Thr Glu Pro Ile Thr Val Lys
195 200 205

Phe Ala Asn Asn Pro Ser Gln Lys Ser Ser Gln Ala Leu Leu Ser Gln
210 215 220

Leu Tyr Gln Ser Pro Asn Arg Arg Tyr Pro Gly Pro Leu His His Gln
225 230 235 240

Ala Gln Arg Phe Arg Leu Asp Asn Leu Leu Asn Met Ala Tyr Gly Val
245 250 255

Lys Arg Leu Met Ser Gly Pro Val Pro Pro Ser Ala Cys Ser Pro Arg

10025357 124901

260	265	270
Phe Ser Pro Ile Thr Ile Asp Gly Met Thr Ser Leu Val Gly Met Asn		
275	280	285
Ile Pro Gly His Thr Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu		
290	295	300
Ser Pro Asp Ser Asp Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe		
305	310	315
Gly Ala Val Asn Asn Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys		
325	330	335
Cys Lys Gly Phe Gly Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala		
340	345	350
Met Ala Ile Ala Ser Leu Asn Gly Tyr Arg Leu Gly Asp Arg Val Leu		
355	360	365
Gln Val Ser Phe Lys Thr Asn Lys Ala His Lys Ser		
370	375	380